

Serial No. 09/807,946
 Amendment Dated January 18, 2007
 Reply to Office Action of October 18, 2006
 APPENDIX B – Sequence Analyses showing conserved domains, motifs, amino acids

PILEUP Multiple Sequence Alignment

Symbol comparison table: blosum62.cmp CompCheck: 1102

GapWeight: 8 GapLengthWeight: 2

BB1410SID4_pileup_121608.txt MSF: 351 Type: P January 5, 2007 10:34
 Check: 7274 ..

BB1410SID6	p0016.ctsas50r corn EST (ELECTED sequence)
BB1410sid8	p0016.ctsas50r corn FIS (ELECTED sequence)
BB1410sid16	scr1c.pk001.d2/ses4d.pk0033.c8 contig soy clones
BB1410sid18	scr1c.pk001.d2 soy FIS
BB1410sid20	ses4d.pk0033.c8 soy FIS/CGS
BB1410sid12	p0083.cldev71r corn EST
BB1410sid14	p0083.cldev71r corn FIS
BB1410SID4	cpilc.pk012.p19 corn FIS/CGS
BB1410sid2	cpglc.pk006.b16/cpilc.pk012.p19 contig corn clones
BB1410sid22	sgs5c.pk0002.f2 soy CGS
BB1410sid24	ssm.pk0060.h4 FIS/NCBI GI#4395781 contig
BB1410sid25	A. thaliani NCBI GI#4090200
BB1410sid10	p0058.chpab57r corn FIS/CGS

FORMATTING to identify conserved regions &/or residues:

Identical or conservative aa residues as compared to SEQ ID NOs: 6&8
 shown in **BOLD** & **Shaded**; Homeobox domain **boxed**

Conservative aa substitutions: McKay et al. (1996) Genomics 36:305-315.
 See Figure 2 legend - (P, A, G, S, T); (E, D, N, Q); (V, I, L, M); (F, W, Y); (R, K, H)

	1	50
BB1410SID6	~~~~~	~~~~~
BB1410sid8	~~~~~	~~~~~
BB1410sid16	~~~~~	~~~~~
BB1410sid18	~~~~~	~~~~~
BB1410sid20	~~~~~	~~~~~
BB1410sid12	~~~~~	~~~~~
BB1410sid14	~~~~~	~~~~~
BB1410SID4	~~~~~	~~~~~
BB1410sid2	~~~~~	~~~~~
BB1410sid22	MKVHQFARG. FWEHEPSLTL GCKRLRPLAP KLSNTDTISP PHHPVTTFDL	
BB1410sid24	MKVHQFTRGL IWEHEPFLTL GCKRLRPLAP KLPNTKTITT P.....FDL	
BB1410sid25	~~~~~	~~~~~
BB1410sid10	~~~~~	~~~~~

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51                                     100
BB1410SID6 ~~~~~~ --MAANAGGG GAGGGSGSGS VAAPAVCRPS GSRWTPTEQ
BB1410sid8 ~~~~~~ --MAANAGGG GAGGGSGSGS VAAPAVCRPS GSRWTPTEQ
BB1410sid16 ~~~~~~ --MESS HSTAEDSGW KGSSGAH.SS VSRWSPTTEQ
BB1410sid18 ~~~~~~ --S HSTAEDSGW KGSSGAH.SS VSRWSPTTEQ
BB1410sid20 ~~~~~~ --MESH SSAPAE... ..NVTRH.SS VSRWSPTTEQ
BB1410sid12 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ Q
BB1410sid14 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ --WATTEQ
BB1410SID4 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ SGRVGKVC... .GRWNPTAEQ
BB1410sid2 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ SGRVGKVC... .GRWNPTAEQ
BB1410sid22 KSFIPKESAS RKLGSSDD NTNKRDPSSP QGQAEITHPG GTRWNPTTEQ
BB1410sid28 KSFIRPESGP RK..FVSSDD ..TKKDPSP QGQIETH.PG GTRWNPTTEQ
BB1410sid25 ~~~~~~ --MEPPQ HQHHHHQADQ ESGNNNNKSG SGGYCRQTS .PRWTPTEQ
BB1410sid10 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ --MEGGLS PERHAAAEFV RSRWTPTEQ

101                                     150
BB1410SID6 IRMLKELYYG CGIRSPSSBQ IQRITAMLRQ HGKIEGKNVF YWFQNHKARE
BB1410sid8 IRMLKELYYG CGIRSPSSBQ IQRITAMLRQ HGKIEGKNVF YWFQNHKARE
BB1410sid16 IDMLENF.YK CGIRTPSTEQ IQQITSRLRA YGIEGKNVF YWFQNHKARQ
BB1410sid18 IDMLENF.YK CGIRTPSTEQ IQQITSRLRA YGIEGKNVF YWFQNHKARQ
BB1410sid20 IDMLENL.YK CGIRTPSTEQ IQQITSRLRA YGIEGKNVF YWFQNHKARQ
BB1410sid12 VAVLEGL.YE HGLRTPSAEQ IQQITGRILRE HGAIEGKNVF YWFQNHKARQ
BB1410sid14 VAVLEGL.YE HGLRTPSAEQ IQQITGRILRE HGAIEGKNVF YWFQNHKARQ
BB1410SID4 VKVLTEL.FR AGLRTPSTEQ IQRISTHLSA FGKVESKNVF YWFQNHKARE
BB1410sid2 VKVLTEL.FR AGLRTPSTEQ IQRISNQLSA FGKGENKNVL LTGPKOKGRE
BB1410sid22 IGLLEML.YR GGMRTFNAAQ IEQITAQLSK YGKIEGKNVF YWFQNHKARE
BB1410sid24 IGLLEML.YK GGMRTFNAAQ IEQITVQLGK YGKIEGKNVF YWFQNHKARE
BB1410sid25 IKILKELYYN NAIRSPADQ IQKITARLRQ FGKIEGKNVF YWFQNHKARE
BB1410sid10 ILILEST.FN SGVNPPKDE TVRIRKLLER FGAVGDANVF YWFQNRRSRS

151                                     200
BB1410SID6 ROKRRLTSLD VNVPAAGAAD ATTSQLGLVLS LSSPPPPSGA. APPS..PTLG
BB1410sid8 ROKRRLTSLD VNVPAAGAAD ATTSQLGLVLS LSSPPPPSGA. APPS..PTLG
BB1410sid16 ROKLQKQQS IAYCNC..FL HASHPICQNV VCVHIVCKR. VDSAFILNQ
BB1410sid18 ROKLQKQQS IAYCNC..FL HASHPICQNV VCAPYCLQK. SGFSFYPHOF
BB1410sid20 ROKL.MKQQT IAYSNR..FL RASHPICQNV ACAPYCLQR. SGFSFYPOQS
BB1410sid12 ROKX.QXACQ L....R.LL QOAPP.PA... .PAAARALH. ABRATVPSRP
BB1410sid14 ROKR..QKQDS FAYFSR..LL RRPPLPLVLS MPPAPPYHH. ARVPAPPATP
BB1410SID4 RHHKKRRRG ASSSSPSGS GRGNNNEEDG RGAAASQHD. ADDADLVLPD
BB1410sid2 RQCKKR~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
BB1410sid22 ROKOKRNNLG LAHSPTTLT ..... TSPPSCCV. ITTMDTKRG
BB1410sid24 ROKOKRSSLA SSHSPPTTI ..... HS..... VVTLETT.RG
BB1410sid25 ROKKRFNGTN MTTFSSSP... .NSVMMAAND HYHPLLHHH. HGVPNQRAN
BB1410sid10 RPRORLOAQ AAASSSSSGS PPTSGLA PGH ATASSTAGMF AHGATYGSSA
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	201		250
BB1410SID6	LYAAGNGGGS	AVLLDTSSDW	GSSGAAMATE
BB1410SID8	LYAAGNGGGS	AVLLDTSSDW	GSSGAAMATE
BB1410SID16	RCLQV	~	~
BB1410SID18	KVLASVIGSS	RIETGSGFML	RICDGMQSE
BB1410SID20	KVLASVIGSS	..TGPIGMO	RMFDGMOSE
BB1410SID22	RP	~	~
BB1410SID14	MPMAPPAA	CNDNGGARVI	YRNPFFVAP
BB1410SID4	PESSKEARS	GHHHRLVTCY	VRDVVEQGEA
BB1410SID2	~	~	~
BB1410SID22	EVEREED	SPLKCRSRW	AFVELEDQ
BB1410SID24	EVERDEBED	SPYKKRCRRW	AFDELEQNM
BB1410SID25	SVNVKLNGDL	HLHYHNMFLPY	SPFNNGINFA
BB1410SID10	SASVPPQDS	EGMMKDLDYG	GDDDLFAHR

	251		300
BB1410SID6	HVRTYELIAA	SFHPVVIIV	RYGGRAPDY MGVTDTGSSS QWPRFSSSDT
BB1410sid8	HVRTYELIAA	SFHPVVIIV	RYGGRAPDY MGVTDTGSSS QWPRFASDDT
BB1410sid16	~~~~~	~~~~~	~~~~~
BB1410sid18	PTGILEKTT	HHSVDVTRKS	FVSIAVDENG HLGNGPCFFN QY ~~~~
BB1410sid20	PTGLIKEKT	HOVFSLASTS	VV..AVDEDG HLGNGPFFNF FTTEPPSRF
BB1410sid12	~~~~~	~~~~~	~~~~~
BB1410sid14	QTVVMYOYR	MEVGAGDKIM	TAAAHACCCO HNGAGOCGR AGHFSRETLQ
BB1410SID4	SYGDLEAAEK	VRSYVRGLAA	TSEQCELSFE FDSVSGRDPP LEIRLCSFGP
BB1410sid2	~~~~~	~~~~~	~~~~~
BB1410sid22	PEGR~~~~~	~~~~~	~~~~~
BB1410sid24	PEGR~~~~~	~~~~~	~~~~~
BB1410sid25	YGSMEQCDSM	NNYNVGWWGA	NMDHHYSASP YNFFDRAKL PLGVGHQBDE
BB1410sid10	HDOOOOYQS	PCQSPASITVE	INGATEVPER GPDILSMFG ODMLHGABSE

[illegible]

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351
BB1410SID6 ~
BB1410sid8 ~
BB1410sid16 ~
BB1410sid18 ~
BB1410sid20 ~
BB1410sid12 ~
BB1410sid14 ~
BB1410SID4 ~
BB1410sid2 ~
BB1410sid22 ~
BB1410sid24 ~
BB1410sid25 N
BB1410sid10 ~

HmmerPfam Results

Query: BB1410SID6 from: 1 to: 238

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
-----	-----	-----	-----	---
Homeobox	Homeobox domain	46.8	5e-10	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
-----	-----	-----	-----	-----	-----	-----	-----
Homeobox	1/1	28	90 ..	1	57 []	46.8	5e-10

Alignments of top-scoring domains:

Homeobox: domain 1 of 1, from 28 to 90: score 46.8, E = 5e-10

		*->rrkRTtftpeQleeLEkeFgk..nrYPsreeReeLakkL....gLte					
		+R+t+tpeQ++ L++++ + r Ps+e++++ ++L++++++					
BB1410SID6	28	SGSRWTPTEQIRMLKELYGcgIRSPSSEQIQRITAMLRqhgKIEG 74					
		rqVkvWFQNRRAKwKk<-*					
		++V++WFQN++a++++					
BB1410SID6	75	KNVFYWFQNHKARERQ 90					

Query: BB1410SID8 from: 1 to: 237

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
-----	-----	-----	-----	---
Homeobox	Homeobox domain	46.8	5e-10	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
-----	-----	-----	-----	-----	-----	-----	-----
Homeobox	1/1	28	90 ..	1	57 []	46.8	5e-10

Alignments of top-scoring domains:

Homeobox: domain 1 of 1, from 28 to 90: score 46.8, E = 5e-10

		*->rrkRTtftpeQleeLEkeFgk..nrYPsreeReeLakkL....gLte					
		+R+t+tpeQ++ L++++ + r Ps+e++++ ++L++++++					
BB1410SID8	28	SGSRWTPTEQIRMLKELYGcgIRSPSSEQIQRITAMLRqhgKIEG 74					
		rqVkvWFQNRRAKwKk<-*					
		++V++WFQN++a++++					
BB1410SID8	75	KNVFYWFQNHKARERQ 90					

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Query: BB1410SID25 from: 1 to: 291 A. thaliani GI 4090200

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
Homeobox	Homeobox domain	44.3	2.7e-09	1
RMMBL	RNA-metabolising metallo- β -lactamase	-5.2	10	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
Homeobox	1/1	34	96	..	1 57 []	44.3	2.7e-09

Alignments of top-scoring domains:

Homeobox: domain 1 of 1, from 34 to 96: score 44.3, E = 2.7e-09

```
*->rrkRTtftpeQleeLEkeFgk..nrYPsreeReeLAkkL...gLte
      +R+t+t+t+Q+++L++++ + r P+++++++ ++L++ +++
BB1410SID2      34      TSTRWTPTEQIKILKELYNNaIRSPTADQIQKITARLrqfgKIEG 80

      rqVkvWFQNRRAKwKk<-*
      ++V++WFQN++a++++
BB1410SID2      81 KNVFYWFQNHKAREQ      96
```